

WHAT IS CLAIMED IS:

- 1        1.     A method of detecting cancer in a patient, the method comprising:  
2                determining the level of a transcript encoding SEQ ID NO:2 in a biological  
3        sample from the patient; and  
4                detecting a decrease in the level of the transcript relative to normal, thereby  
5        detecting the presence of cancer in the patient.
- 1        2.     The method of claim 1, wherein the cancer is selected from a group  
2        consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.
- 1        3.     The method of claim 1, wherein the step of determining the level of the  
2        transcript comprises an amplification reaction.
- 1        4.     A method of detecting cancer in a patient, the method comprising:  
2                determining the level of a polypeptide having the sequence set forth in SEQ  
3        ID NO:2 in a biological sample from the patient; and  
4                detecting an increase in the level of the polypeptide relative to normal, thereby  
5        detecting the presence of cancer in the patient.
- 1        5.     The method of claim 4, wherein the cancer is selected from the group  
2        consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.
- 1        6.     The method of claim 4, wherein the step of determining the level of the  
2        polypeptide comprises performing an immunoassay.
- 1        7.     A method of detecting cancer in a patient, the method comprising:  
2                determining the amount of methylation of a SOCS-3 promoter in a biological  
3        sample from the patient; and  
4                detecting an increase in the amount of methylation of the sample relative to  
5        normal, thereby detecting the presence of cancer in the patient.
- 1        8.     The method of claim 7, wherein the amount of methylation of the CpG  
2        residues that occur within the region from -1005 to -983 or from -754 to -737 of SEQ ID  
3        NO:3 is determined.

1                   9.       The method of claim 7, wherein the amount of methylation of the  
2       SOCS-3 promoter is determined using bisulfite sequencing.

1                   10.      The method of claim 7, wherein the amount of methylation of the  
2       SOCS-3 promoter is determined using methylation-specific PCR.

1                   11.      The method of claim 7, wherein the amount of methylation is detected  
2       using a methylation-sensitive restriction enzyme.

1                   12.      A method of monitoring the efficacy of a therapeutic treatment of  
2       cancer, the method comprising the steps of:

3                   (i) providing a biological sample from a patient undergoing the therapeutic  
4       treatment; and

5                   (ii) detecting the level of: a polypeptide having an amino acid sequence of  
6       SEQ ID NO:2, or of a nucleic acid that encodes the polypeptide, in the biological sample  
7       compared to a level in a biological sample from the patient prior to, or earlier in, the  
8       therapeutic treatment, thereby monitoring the efficacy of the therapy.

1                   13.      A method of monitoring the efficacy of a therapeutic treatment of  
2       cancer, the method comprising the steps of:

3                   (i) providing a biological sample from a patient undergoing the therapeutic  
4       treatment; and

5                   (ii) detecting the level of methylation of the SOCS-3 promoter in the  
6       biological sample compared to a level in a biological sample from the patient prior to, or  
7       earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

1                   14.      A method of screening for an agent that increases SOCS-3 activity, the  
2       method comprising

3                   incubating a test compound with a cell comprising a SOCS-3 nucleic acid  
4       having at least 80% identity to SEQ ID NO:1;

5                   selecting a compound that increases SOCS-3 activity, thereby identifying an  
6       agent that increases SOCS-3 activity.

1                   15.      The method of claim 14, wherein the SOCS-3 nucleic acid sequence  
2       further comprises a hypermethylated promoter.

1                   16. The method of claim 15, further comprising a step of determining the  
2 amount of methylation of the SOCS-3 promoter following incubation with the test  
3 compound.

1                   17. The method of claim 14, wherein the increase in SOCS-3 activity is  
2 determined by measuring the level of SOCS-3 mRNA transcript.

1                   18. The method of claim 14, wherein the increase in SOCS-3 activity is  
2 determined by measuring the level of SOCS-3 polypeptide.

1                   19. A method of inhibiting proliferation of a cancer cell, the method  
2 comprising administering an agent that increases SOCS-3 activity to the cancer cell.

1                   20. The method of claim 19, wherein the cancer cell has a hypermethylated  
2 SOCS-3 promoter.

1                   21. The method of claim 20, wherein the cancer cell is selected from the  
2 group consisting of a lung cancer cell, a breast cancer cell, a mesothelioma cell, a colon  
3 cancer cell, and a sarcoma cell.

1                   22. The method of claim 19, wherein the agent is an expression vector  
2 encoding SOCS-3.

1                   23. The method of claim 19, wherein the agent is recombinant SOCS-3.

1                   24. The method of claim 19, wherein the agent is a demethylating agent.

1                   25. A kit comprising methylation-specific primers that are selective for  
2 methylated residues present within the region from -1005 to -983 or from -754 to -737 of  
3 SEQ ID NO:3.